



## SEQUENCE LISTING

<110> CENTRE NATIONAL DE LA RECHERCHE SCIENTIFIQUE - CNRS

<120> CLONING, EXPRESSION AND CHARACTERIZATION OF THE SPG4  
GENE RESPONSIBLE FOR THE MOST COMMON FORM OF AUTOSOMAL  
DOMINANT SPASTIC PARAPLEGIA

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## SEQUENCE LISTING

<110> CENTRE NATIONAL DE LA RECHERCHE SCIENTIFIQUE - CNRS

<120> CLONING, EXPRESSION AND CHARACTERIZATION OF THE SPG4  
GENE RESPONSIBLE FOR THE MOST COMMON FORM OF AUTOSOMAL  
DOMINANT SPASTIC PARAPLEGIA

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 gtatcgaaga actggaaaaa ggaatcgctg ttatagttac gggccaagggt gaacagtatg 180  
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 aagacttgaa aaatttttagg aatgtggaca gcaatcttgc taaccttata atgaatgaaa 660  
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&lt;211&gt; 504

&lt;212&gt; PRT

&lt;213&gt; mouse

&lt;220&gt;

&lt;223&gt; Incomplete murine spastin.

&lt;400&gt; 73

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Ala Glu Ser Val Arg Val Phe His Lys Gln Ala Phe Glu Tyr Ile Ser
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Ile Ala Leu Arg Ile Asp Glu Glu Glu Lys Ala Gly Gln Lys Glu Gln
      20              25              30

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Ala Val Glu Trp Tyr Lys Lys Gly Ile Glu Glu Leu Glu Lys Gly Ile
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Ala Val Ile Val Thr Gly Gln Gly Glu Gln Tyr Glu Arg Ala Arg Arg
      50              55              60

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Leu Gln Ala Lys Met Met Thr Asn Leu Val Met Ala Lys Asp Arg Leu
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Gln Leu Leu Glu Lys Leu Gln Pro Val Leu Gln Phe Ser Lys Ser Gln
      85              90              95

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Thr Asp Val Tyr Asn Glu Ser Thr Asn Leu Thr Cys Arg Asn Gly His
      100             105             110

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Leu Gln Ser Glu Ser Gly Ala Val Pro Lys Arg Lys Asp Pro Leu Thr
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His Ala Ser Asn Ser Leu Pro Arg Ser Lys Thr Val Leu Lys Ser Gly
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Ser Ala Gly Leu Ser Gly His His Arg Ala Pro Ser Cys Ser Gly Leu
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 His Lys Gly Thr Pro Lys Pro Asn Arg Thr Asn Lys Pro Ser Thr Pro  
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 Thr Thr Ala Val Arg Lys Lys Lys Asp Leu Lys Asn Phe Arg Asn Val  
 195 200 205  
 Asp Ser Asn Leu Ala Asn Leu Ile Met Asn Glu Ile Val Asp Asn Gly  
 210 215 220  
 Thr Ala Val Lys Phe Asp Asp Ile Ala Gly Gln Glu Leu Ala Lys Gln  
 225 230 235 240  
 Ala Leu Gln Glu Ile Val Ile Leu Pro Ser Leu Arg Pro Glu Leu Phe  
 245 250 255  
 Thr Gly Leu Arg Ala Pro Ala Arg Gly Leu Leu Leu Phe Gly Pro Pro  
 260 265 270  
 Gly Asn Gly Lys Thr Met Leu Ala Lys Ala Val Ala Ala Glu Ser Asn  
 275 280 285  
 Ala Thr Phe Phe Asn Ile Ser Ala Ala Ser Leu Thr Ser Lys Tyr Val  
 290 295 300  
 Gly Glu Gly Glu Lys Leu Val Arg Ala Leu Phe Ala Val Ala Arg Glu  
 305 310 315 320  
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 325 330 335  
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 340 345 350  
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 355 360 365  
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 370 375 380  
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 385 390 395 400  
 Thr Arg Leu Leu Leu Leu Lys Asn Leu Leu Cys Lys Gln Gly Ser Pro  
 405 410 415  
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 420 425 430  
 Ser Gly Ser Asp Leu Thr Ala Leu Ala Lys Asp Ala Ala Leu Gly Pro  
 435 440 445  
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 450 455 460

Met Arg Asn Ile Arg Leu Ser Asp Phe Thr Glu Ser Leu Lys Lys Ile  
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